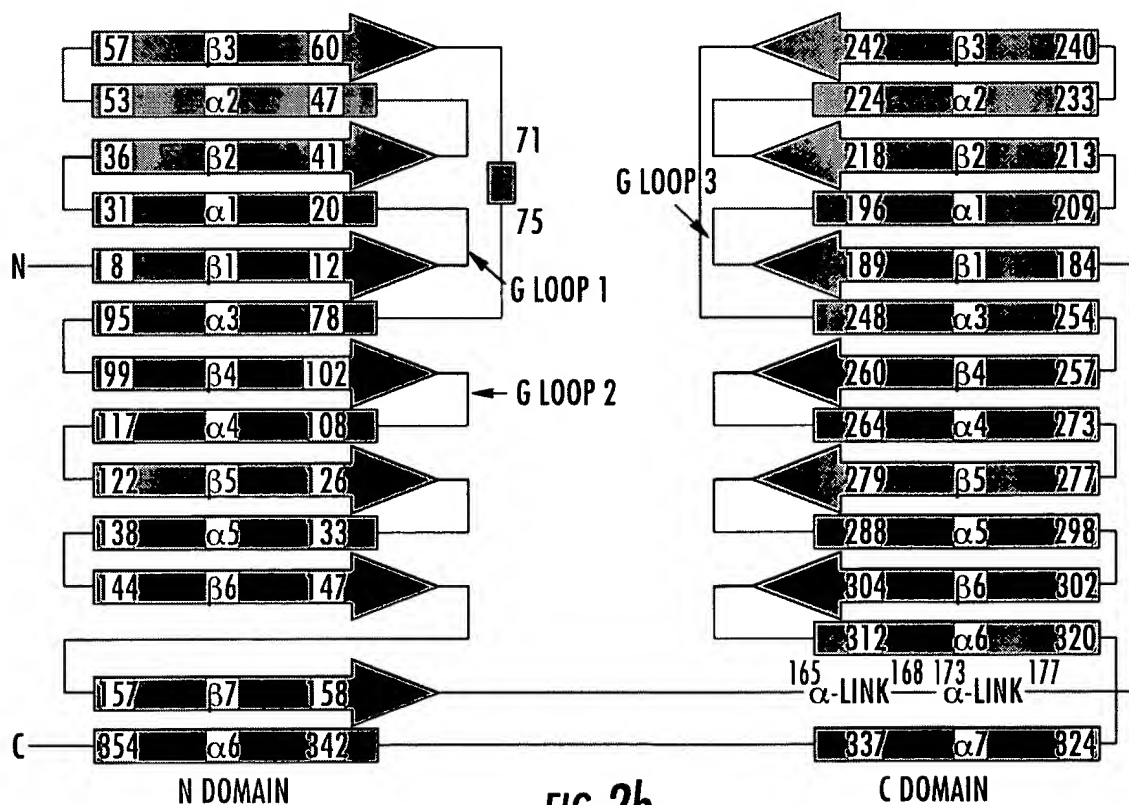
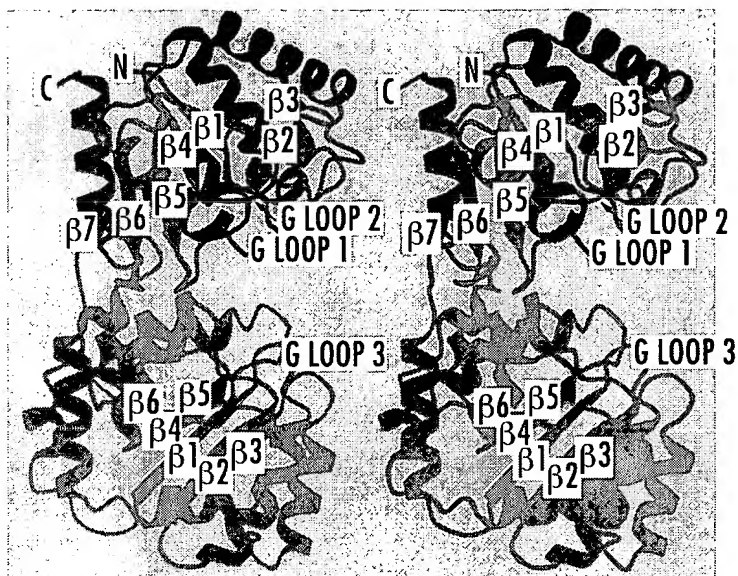


FIG. 2a

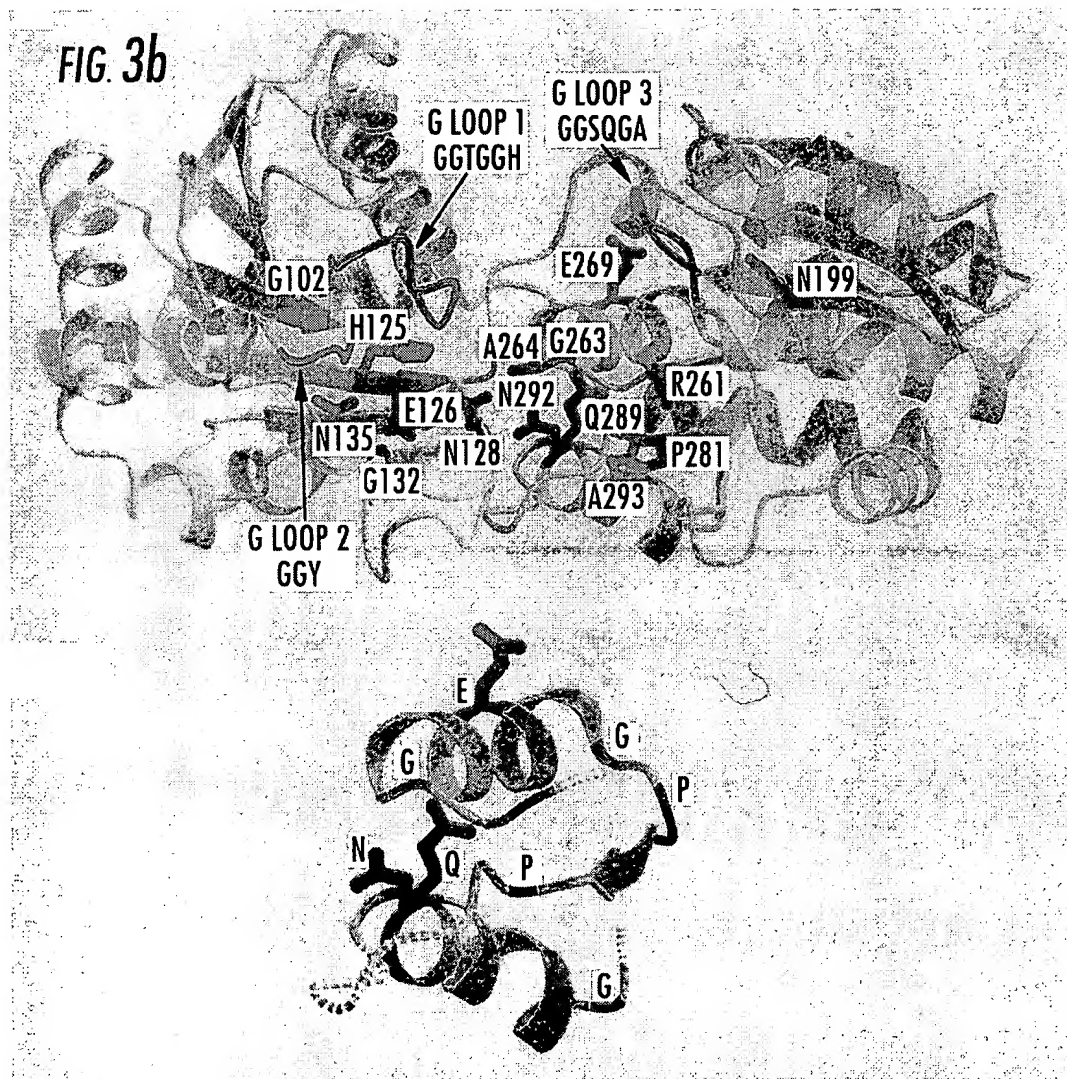




E. COLI	LG-----	IPVVLHEQNGIAGLTKWKLAKIAKVMQAPGCA-----	FPNAEVV--GHPVTDVLALPQQLAGL-----	EGYVRVLVV--GSGQCARLNMQTHQVAAKLGDS--YTIWHQSGKSGSQ
HAEMOPHILUS INFLUENZAE	CG-----	VPITLHQNAIAGLTKWKLGIATCVLQAPPA-----	PPHAENV--GHPVEDLFPHPNDIRFSDR-----	EEKLARLVV--GSGQCARVLNHTLPKVVAQLADK--LEFRHQVQKGAV
ENTEROCOCCUS FAECALIS	-----	HQLKPTTIIHQNSITPGTKTFLSRVVDKIAICPPDVASF--	FPKCKTILGSPGQGVWVTKGAIL-----	DPKAKTVLTVGGSGCALKINQAFQAPLFEEREYQVTVASGERY
ENTEROCOCCUS HIRAE	-----	SKLAIPRTIIHQNSVPGTKTFLSRVDRIALSPEDAAPP--	PPAEKSGSLGNPRAQEVADMNKSIL-----	DPKKTVTLTVGGSGCALKINQAFVFLMSFDQ--EYQVTVASGERY
STREPTOCOCCUS PNEUMONIAE	SG-----	VPVTVIHESDLSGSLGKATKATKFAKTVSTEQDASSL-----	KYEHVGAVTVKSDQNGPDELVDIQSH-----	NHKLTVPLVGGSGACARFNQVLVTDHKKELTER--YVLINLWGDSSL
RICICETTESTA PROWAEKII	-----	LRPTIIHQNSVLGKVFQKFAFKAIKNSYDVKLPFAKSVIL	FGGIVTKVRKIRLSDSPWSVQSLSFKLTQATLTTFPVLV	FGKGRDIFANSITFTIFIGSGAGAKFSELLPAKIKLMKQPSLENIIQGAA
BACILLUS SUBTILIS	-----	AKMGIPRTIIHQNSLPGTKTFLSKYVNKVAICPEEAKSH--	FPSEKVVTFGNPRASEWWSIKTGRSL-----	AEPKL-----SEDKTIVLTVGGSGCAAPINRAVDIMQVLTATKYDQVLYTGVHY
COBACTERIUM TUBERCULOSIS	LPFP	RRRRRRPVPWHEANARAGLANRYGAFTDVLVSAPVDSG--	LRAEVV--GYPVRASIALDLRAVLK-----	AEARAHGFPDDARVLTVGGSGQCARSLNRAVSGAAADLAAGVCLVHAGPQNV
CONSENSUS		P HEON G NK A	G P	L
			GGSQCA LN	

QVSEQVAE---AQOPHQVTEFD--MAAYAWADVVCISGALTWSIAAGLPALIVPF--QH-KROQYVNALPIETAGAKALIEQOLSDVAVANTLAG--WSRETLTWAERARARASIPDATERVANEVSKVARALEHHHHH
EVSQVLGE---NLE-QVKITEFDN--MEAYAWADVVCISGALTVOEIAAGAAITVPF--QH-KROQYVNALXIVSOVGAALIEQADUTPEILVNVLN--LTRENILQALAKANTWMPNWAQVAVIKOYSN
QELQESLK-ISEKLTIVSQVYIDK--WVEYEWANTDLWCRAGATSIAETPALGPAILIPS--PYVYTHQTKWASQVLWVGAVEMIPDAETGARGVAAIDDDILLANNEKROQMATASGERIPDASDRLYQWKTIV
KOIQTKVP-AC-----ANVSIQPYINK--MAEYAWSSDLVWCRAGATSIAETPALGPAILIPS--PYVYTHQTKWASQVLWVNAWAKIKODELDGRLSKQALIEETVTDQLOQMSLASQOQIPDASERVELVQSLIQ
NELSNL-----FRV--PYVYTDYDQ--LEMLADIVTWGAGANTIFELLATAKLHIVVPLGKREASGOQLENAAYPVKKVYADIEQESDITDSLEELKSHLLSHKEDYQAKWASKEL-----KSLADFPVQLLKJLUS
LDHQVTKIDYISKLNIYTFEPFDFDN--IALQVKYANVIVCRAGASTIAETITGLPAITPL--PSAANDHQYVNAKLENDONTAGWCLEQONTSSKXIAOKILDISHROQLLED---ASQNLNNEKEGCHVLLSNLIEDIVFL
EKVWNEUK--SKGADWNTKFPFLHQ--MPEYKALDIVIVARAGASTIAETITAGLIPSVLIPS--PYVYTHQYVNAKLSGQHDAAIVLVKETPLSGEKLIEALORIVLNEQTLKEMSERITSISGLVPDAAALIVSVLEELKX
LELRER-----AQGDDPPYVAVPYLDR--MELAYAAADIVICRAGANTVAVSAGVCLPAIVPL--PI--CGEGRNLNLPVWNGKGGWVADALITVELVAVQAGLLITPDRLAANTAAARVCHRDGAGOVARAALAVACAGATTFT
CONSENSUS
F M D R G A T E G P A P Q N A G L A
HxGxxxxxxExxxxGxPxxxxPxF-----xxQxNxxxxxxxGx
UDP--GLUCURONOSYLTRANSFERASE CONSENSUS REGION

FIG. 3A



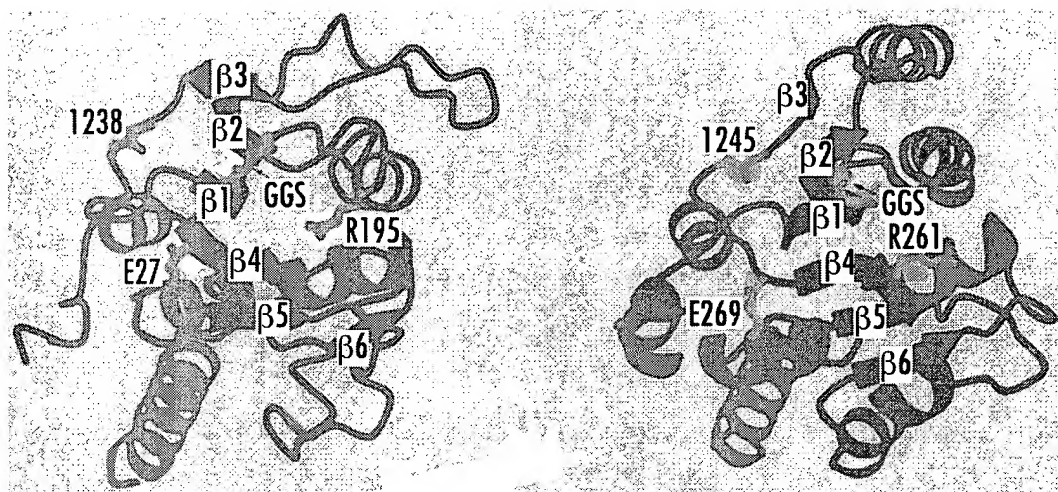


FIG. 4A

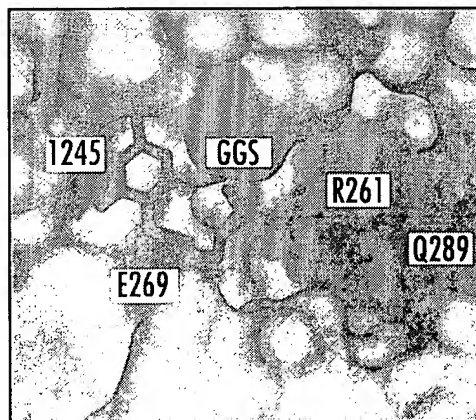


FIG. 4B

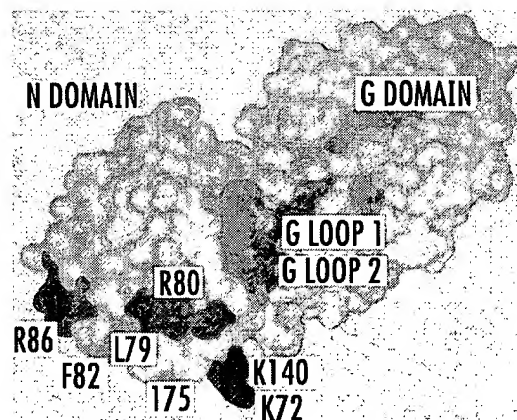


FIG. 4C